



Ct values:

What do they mean?

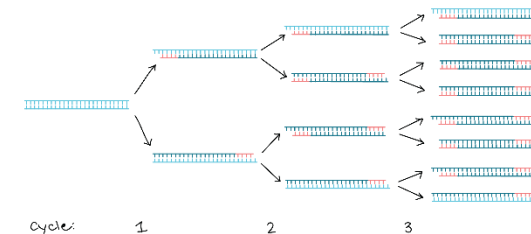
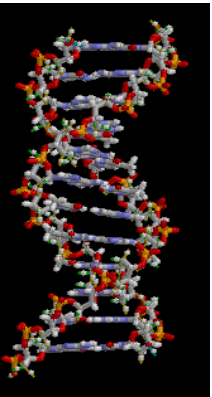
Can they be used?

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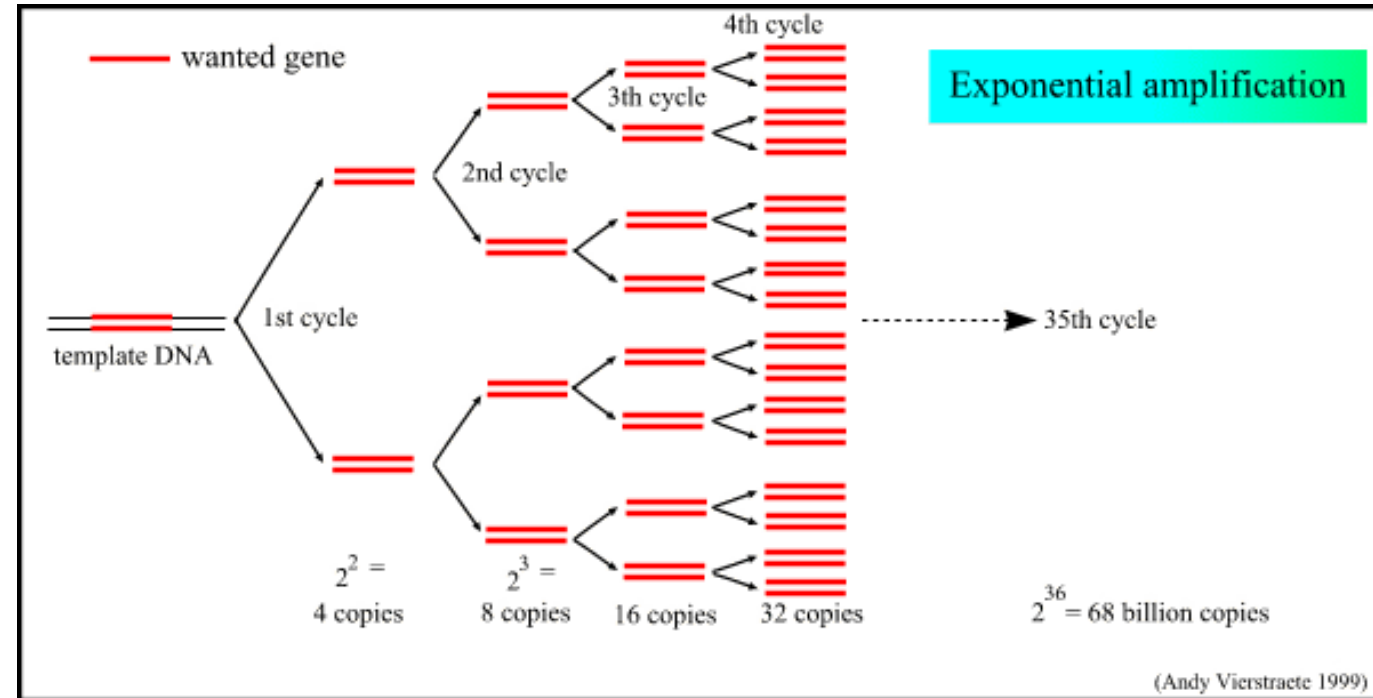
University of Nevada, Reno School of Medicine



PCR is a method of amplifying a target DNA molecule

-For SARS-CoV-2, the target is the virus' genome; ---it is made of RNA; but it is an easy process to convert RNA into DNA

-PCR takes place in **cycles**; each cycle, temperature is changed from cold to hot to warm and then back to cold.



With each cycle, the amount of target (theoretically) doubles. This is **amplification**, and gives PCR its extreme sensitivity

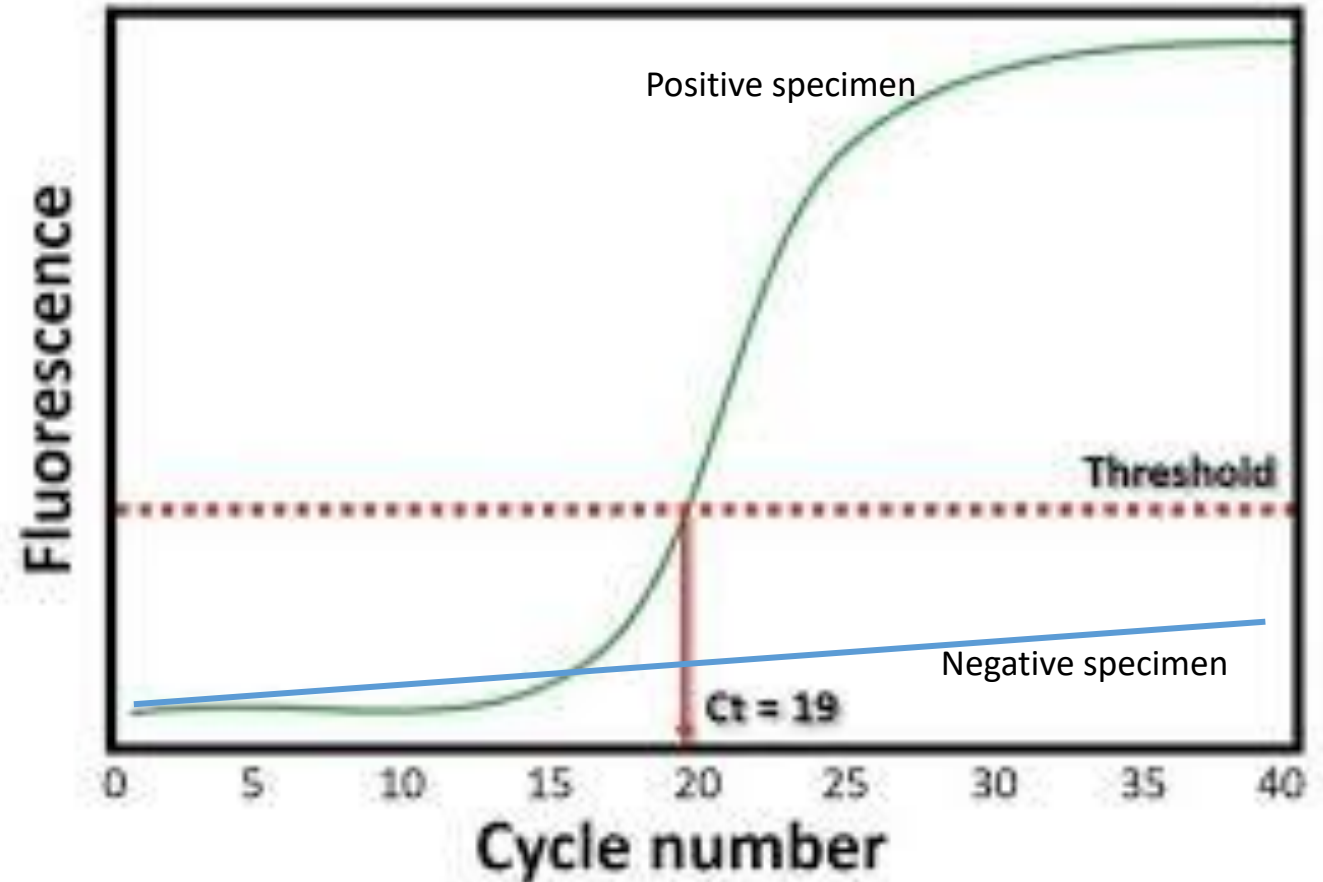
PCR

--With each cycle, if target is present, the amount of target is (essentially) doubled

--amplified targets are measured by fluorescent light that they give off

--"positive" and "negative" specimens are differentiated by whether the amount of fluorescent light given off passes a threshold

--The cycle where that amount of fluorescence is reached is a "Ct" or "Cycle threshold".



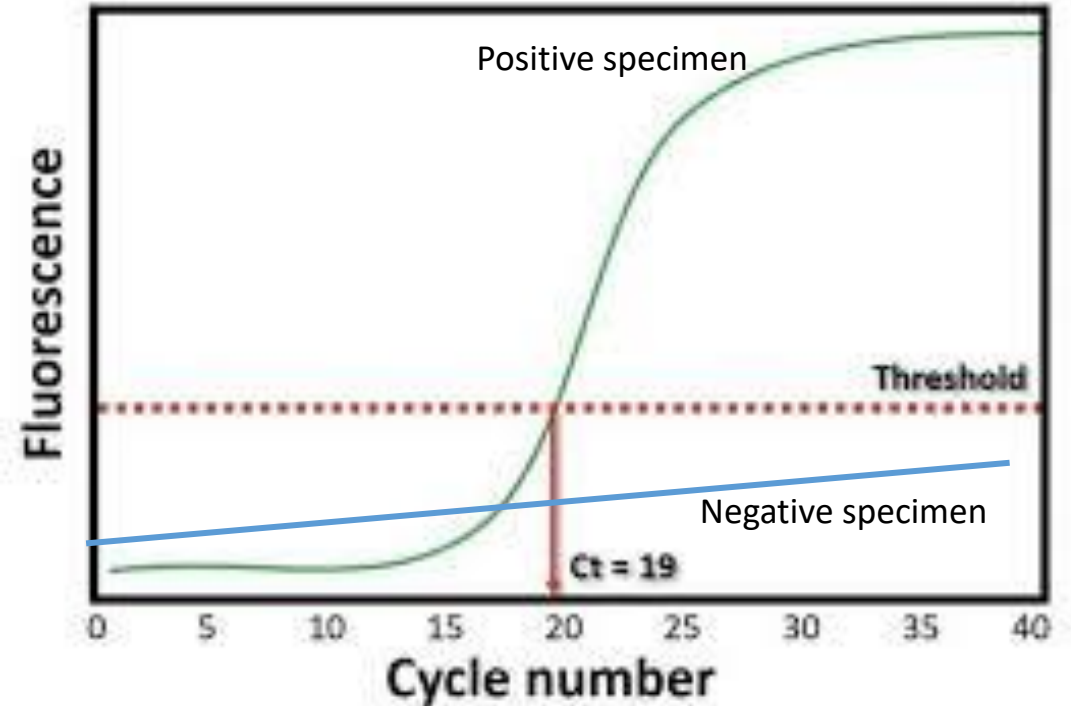
PCR

--lab tests therefore use Ct value as a measure of whether to call a specimen Positive or Negative

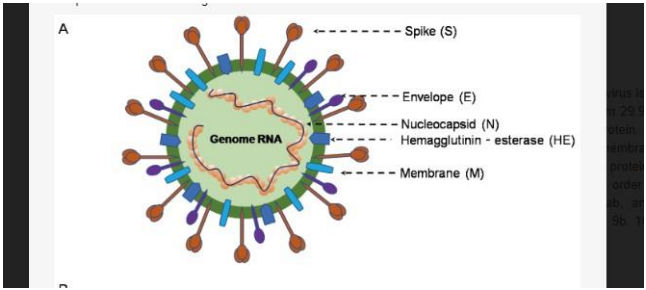
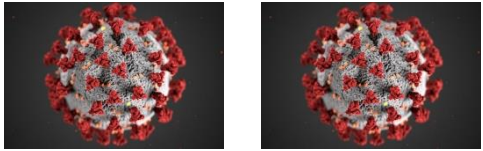
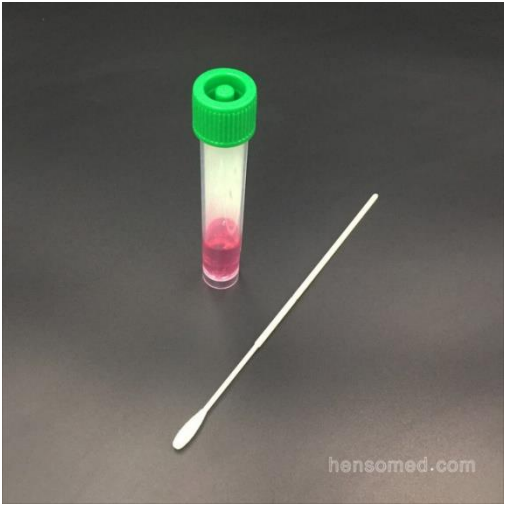
--low Ct values are achieved when there is a large amount of target present; high Ct values are achieved when there is a low amount of target present

--think of Ct as a measure of “*effort*” that the test has to make to detect a positive specimen:

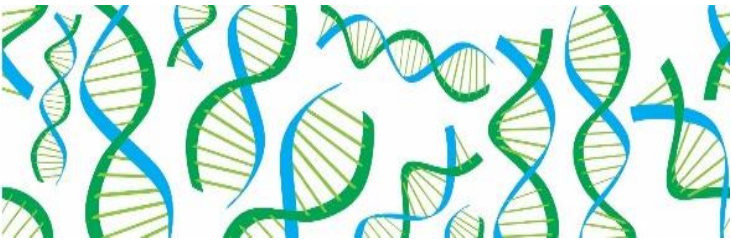
if there is very little target (**virus**) in the sample, then you have to do *a lot* of cycles of amplification to find it; and vice versa



PCR testing, the components:



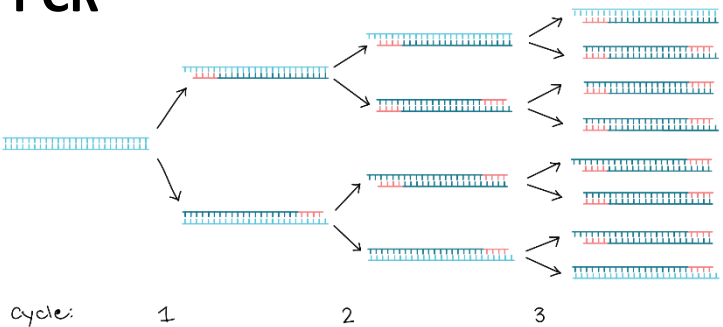
RNA (viral genome) extraction



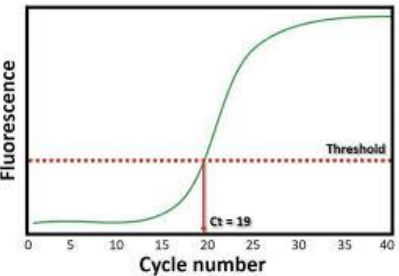
Convert all RNA to DNA



Amplify by
PCR



Positive or Negative
Result
based on Ct value



Ct values correlate with a specimen's ability to infect cells in laboratory culture

- La Scola B, Le Bideau M, Andreani J, Hoang VT, Grimaldier C, Colson P, Gautret P, Raoult D. Viral RNA load as determined by cell culture as a management tool for discharge of SARS-CoV-2 patients from infectious disease wards. **Eur J Clin Microbiol Infect Dis**. 2020 Jun;39(6):1059-1061. doi: 10.1007/s10096-020-03913-9. Epub 2020 Apr 27. PMID: 32342252; PMCID: PMC7185831.
- Jefferson T, Spencer EA, Brassey J, Heneghan C. Viral cultures for COVID-19 infectious potential assessment - a systematic review. **Clin Infect Dis**. 2020 Dec 3:ciaa1764. doi: 10.1093/cid/ciaa1764. Epub ahead of print. PMID: 33270107.
- Bullard J, Dust K, Funk D, Strong JE, Alexander D, Garnett L, Boodman C, Bello A, Hedley A, Schiffman Z, Doan K, Bastien N, Li Y, Van Caeseele PG, Poliquin G. Predicting infectious SARS-CoV-2 from diagnostic samples. **Clin Infect Dis**. 2020 May 22:ciaa638. doi: 10.1093/cid/ciaa638. Epub ahead of print. PMID: 32442256; PMCID: PMC7314198.
- Laferl H, Kelani H, Seitz T, Holzer B, Zimpernik I, Steinrigl A, Schmoll F, Wensch C, Allerberger F. An approach to lifting self-isolation for health care workers with prolonged shedding of SARS-CoV-2 RNA. **Infection**. 2020 Oct 6:1–7. doi: 10.1007/s15010-020-01530-4. Epub ahead of print. PMID: 33025521; PMCID: PMC7538033.
- CDC, unpublished data
- I've personally done this/seen this myself, here at the NV State Public Health Lab

What is “culture”?

→ Another kind of lab test

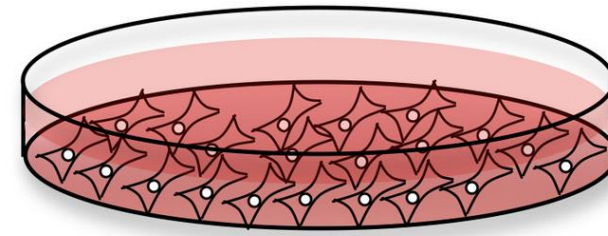
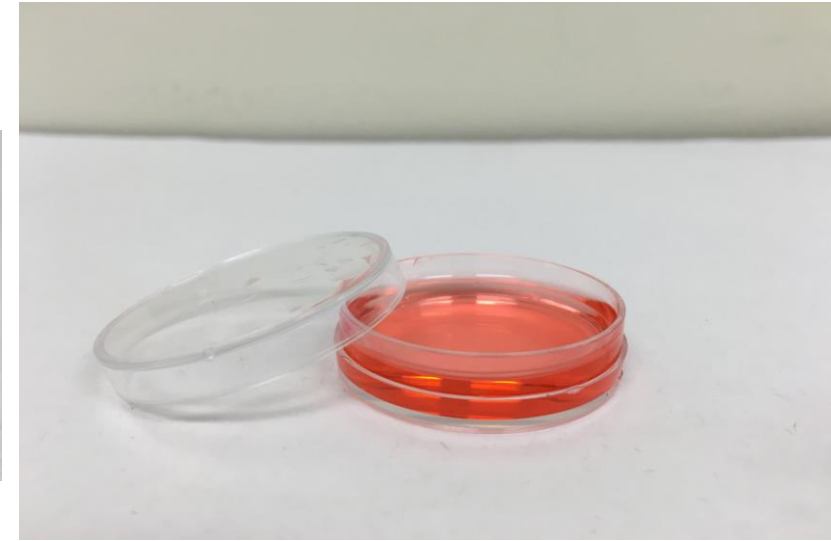
--**infectious** virus can be detected using what are called “cell culture” techniques

--Cell culture involves using cells derived from humans or animal tissue that is / was cancerous

--cancer cells live forever in culture

--viruses can be **detected** / **propagated** by adding them to cell cultures

--“Vero” cells are commonly used for **SARS-CoV-2** infection/propagation



Cells grow adherently to bottom of dish

Vero cells: African Green Monkey Kidney cancer: have been growing since 1962;

“high” Ct specimen don’t grow in culture

--low amount of virus?

--“broken”, junk particles?

-CDC showed no ability to infect cells in Vero
culture after Ct value 33.00 (on *their* PCR assay)

So...

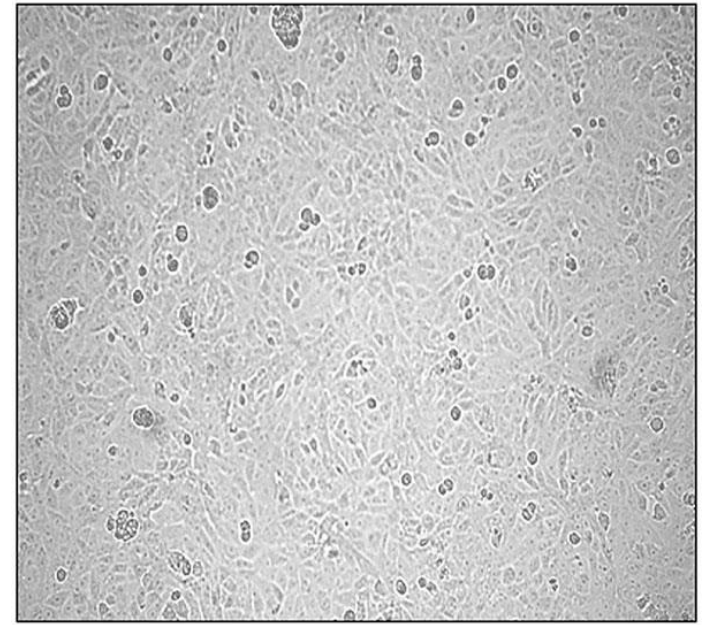
--do such specimens present a public health threat?

--do PCR assays go too far?

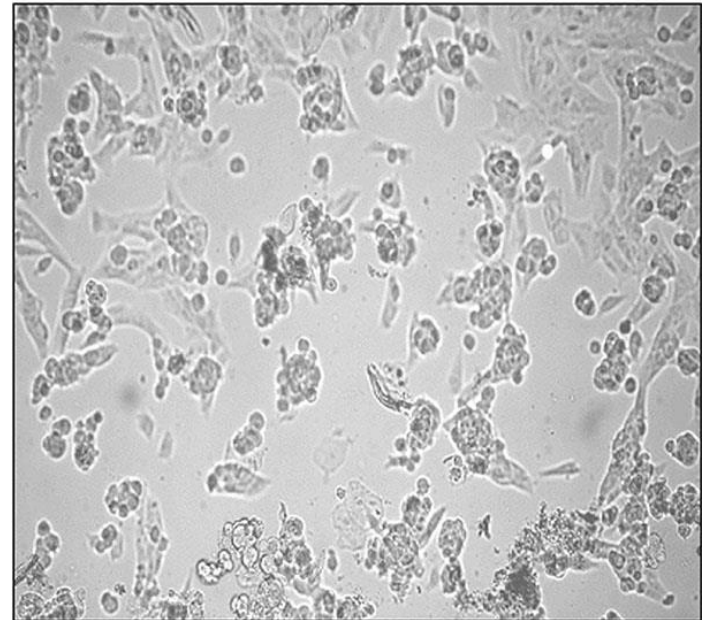
No commercial or CDC assay used in
Nevada with EUA uses cutoffs higher
than 40.

Uninfected cells

A



B



Infected

Ct values are not ready to be
used diagnostically, or routinely

Seven considerations in this regard, follow:

1. Different assays, different Ct

--NSPHL Ct data between two assays

--efficiencies of PCR vary

--where would you draw the line?

--e.g. what would you say about Ct
values of, say, 32 or 34, *if your cutoff
was 33?*

TaqPath Thermofisher		TaqPath CDC	
Sample	N gene	N1	N2
39954	35.2437	35.7	41.29
39956	21.6744	23.15	22.05
39958	0	0	0
39959	0	0	0
39960	0	0	0
39961	27.5361	29.39	29.64
39962	26.5438	27.48	28.29
39963	0	0	0
40317	31.4505	29.71	30.54
40318	0	0	0
40319	0	0	0
40321	0	0	0
40322	30.6259	29.03	29.46
40459	28.1731	27.82	28.57
40460	31.5004	30.767	32.85
40461	22.3216	21.38	22.44
40462	0	0	0
40463	0	0	0
40464	21.397	20.44	21.08

40% of specimens show >4-fold difference in load (i.e.
greater than 2 Ct differences)

2. Extraction methods affect Ct values

-swabs pulled out of noses and throats have viral loads on them

-to measure it, the viruses must be destroyed and their RNA molecules removed

-the RNA is removed, and ‘washed’ for PCR to follow

-this is called “extraction”

-there are many kits on the market for this

gene target	Qiagen Viral Mini Kit	MagMAX Viral NA Iso Kit	Mag-Bind Viral NA Extraction Kit
N1	19.579	19.33	21.19
N2	19.84	19.46	21.53
N1	19.56	19.97	21.07
N2	19.82	20.08	21.25
N1	20.8	22.45	24.4
N2	22.57	22.26	24.08
N1	27.04	27.33	30.78
N2	29.03	28.37	31.82
N1	14.86	15.57	16.98
N2	15.85	15.32	16.98
N1	34.65	0	0
N2	36.72	38.35	0
N1	17.12	17.66	18.64
N2	17.38	17.55	18.31
N1	26.66	26.2	28.76
N2	27.34	25.93	28.75
N1	29.07	30.22	31.18
N2	28.47	31.44	32.13
N1	33.96	34.11	35.7

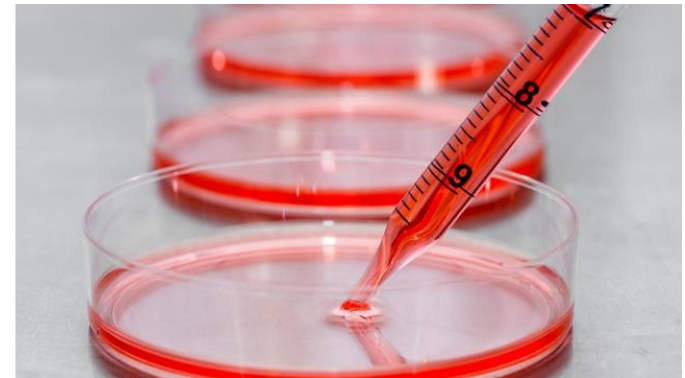
Arrows indicate where different extraction methods led to different Ct values from the SAME specimens in the final PCR by at least a factor of 2 (est: a 4-fold change in measured viral load)

3. Is lab cell culture a proper surrogate for the real infectious process?

--cancer cells in a dish vs. primary human systems: are they equal ?

--evolution of SARS-CoV-2 occurs(ed) in real tissue, not in cell cultures

--very hard to do actual infectivity experiments without volunteer human subjects



We don't know yet. For other viruses (e.g. HIV), there are vast differences in infectivity

4. Collection and storage variability can cause Ct variability

Keep in mind:

What is tested by PCR may not reflect what was in the nose at the time of collection:

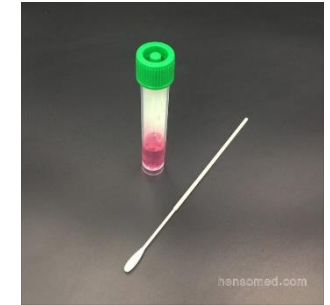
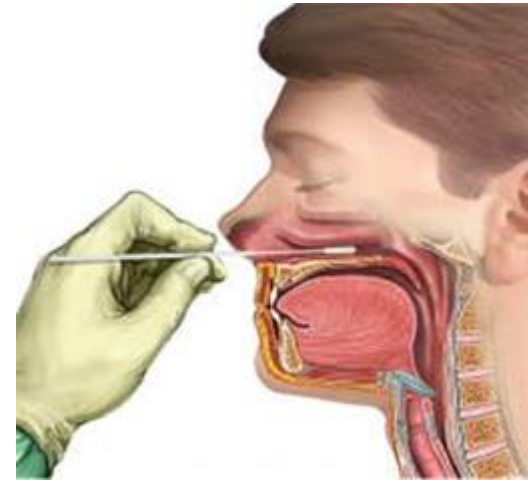
After collection, specimens are put into media, stored for 1-3 days, at room temperature or cold packs, sometimes they are transported long distances

So: what was an infectious virus at time of collection, may not be after PCR testing has occurred

Lots of handling steps.

PCR / Ct generation

RNA Extraction



1-3 days

5. Most positive specimens detected are in an “infectious” Ct range

--pandemic was not caused by high Ct values

--sampling 1,264 specimens from our CDC assay data*:

mean Ct: **27.55**

SD: **6.11**

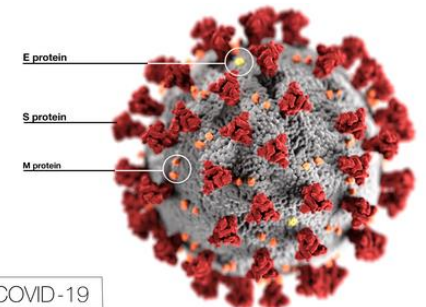
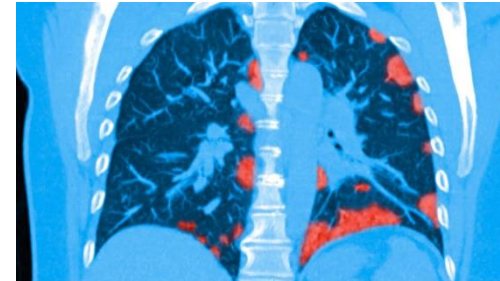
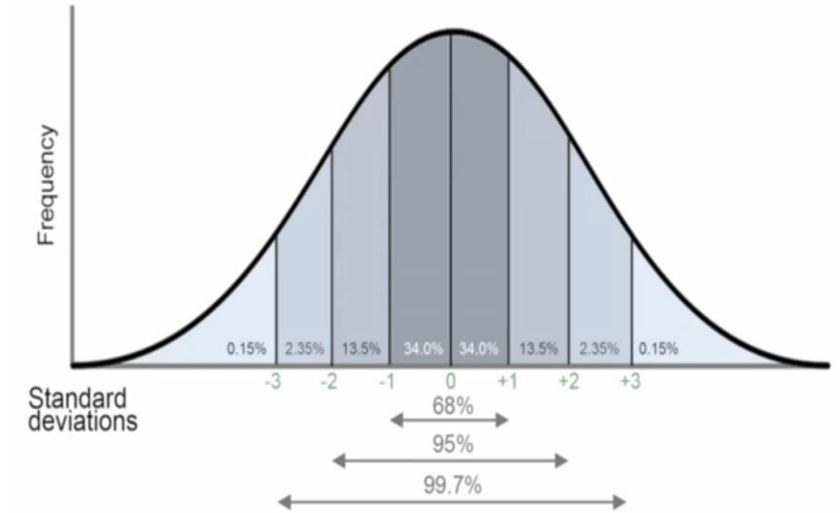
So: ~**84%** of specimens tested have had a Ct value *less than* **33.66**.

According to CDC data, this means that

The strong majority of specimens we have

ascertained at NSPHL likely *were infectious* in cell culture

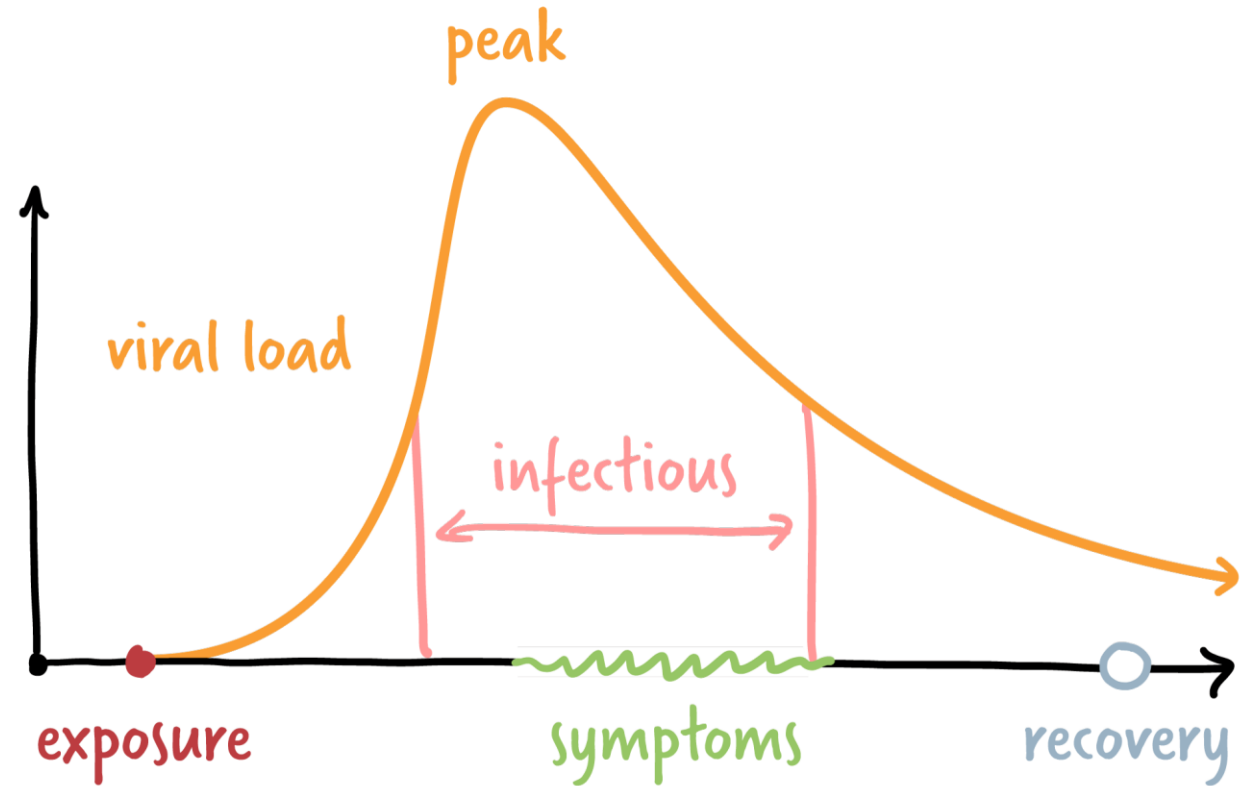
*using N-gene detection



6. Note: viral load doesn't tell you whether infection is new or old

--high Ct, low load specimens can be "coming" or "going"

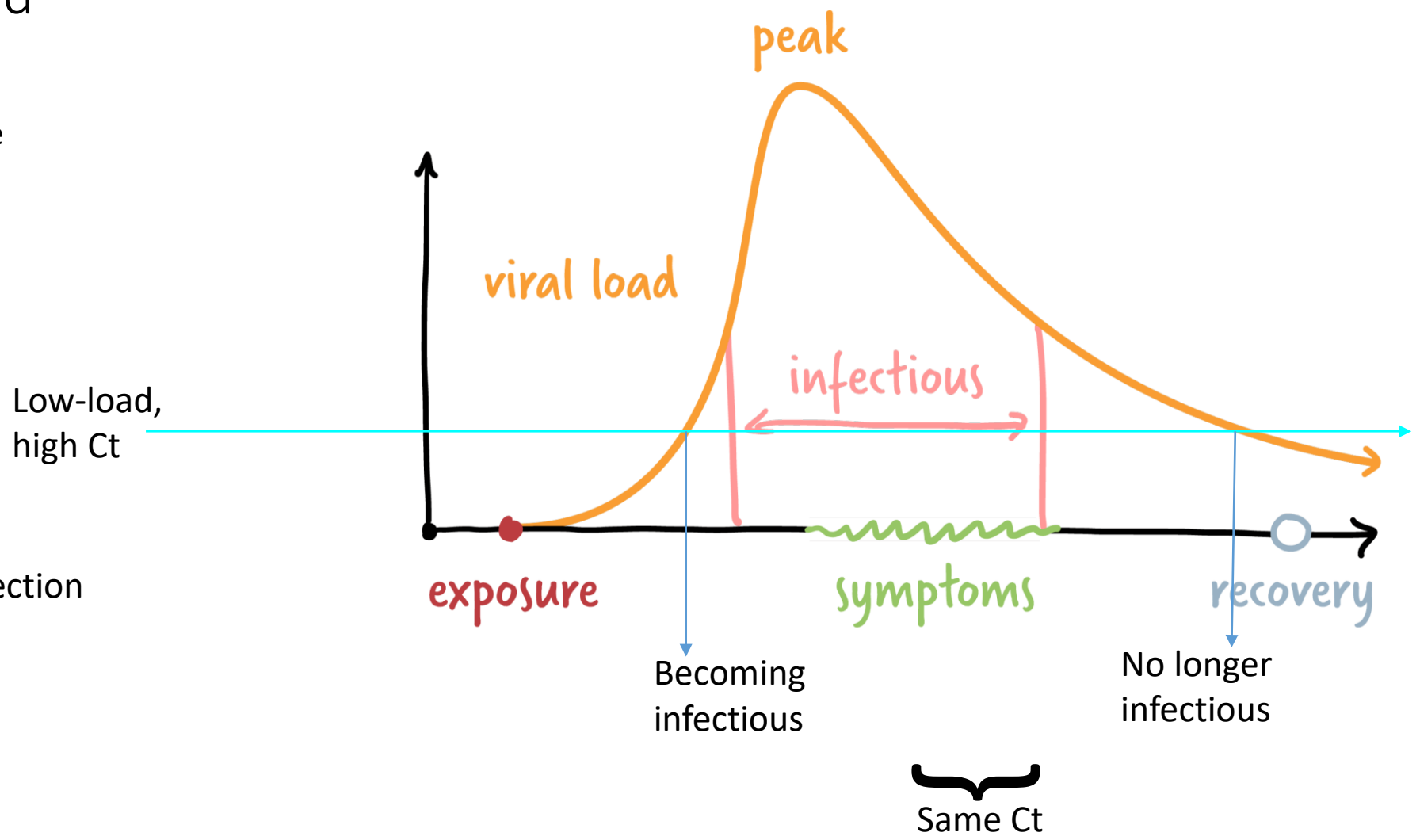
-misclassification of a new infection as an old infection could be catastrophic



6. Note: viral load doesn't tell you whether infection is new or old

--high Ct, low load specimens can be "coming" or "going"

-misclassification of a new infection as an old infection could be catastrophic



7. Published Work showing Ct values >36 *can* harbor infectious virus

- Romero-Gómez MP, Gómez-Sebastian S, Cendejas-Bueno E, Montero-Vega MD, Mingorance J, García-Rodríguez J; SARS-CoV-2 Working Group. **Ct value is not enough to discriminate patients harbouring infective virus**. *J Infect*. 2020 Nov 26:S0163-4453(20)30720-9. doi: 10.1016/j.jinf.2020.11.025. Epub ahead of print. PMID: 33248218; PMCID: PMC7688433.
- -they show that perhaps timing of specimen collection after symptoms can affect infectivity of specimen

What is going to happen ?

- Truth: there is a correlation with infectivity!

Potential ways forward:

- Standardization of viral loads
- Antigen tests as “clearance” tests?
- Per-assay cutoffs?
- Whatever it is, the FDA will have a major say in how and when!

